CRADA Opportunity: New Method for Detection of Highly Pathogenic Salmonella

Salmonella enterica is a leading agent of gastrointestinal illness in the US and worldwide. Salmonella are a diverse group of bacteria with over 1,700 serotypes noted for causing human illness. But while any Salmonella may make the right host sick when present at the right dose, only 15 serotypes are responsible for over two-thirds of documented illnesses in the U.S. each year. These top ranked Salmonella are able to infect more people, in part because of their virulence gene repertoire and a resultant decreased minimal infective dose.

US Meat Animal Research Center scientists conducted comparative genomic analyses of a variety of *Salmonella* strains associated with humans and cattle. These analyses revealed molecular targets for identifying four of the leading disease-causing *Salmonella* serotypes (Enteritidis, Typhimurium, (1,4,[5],12:i:-), and Newport) and a noted invasive serotype, *S.* Dublin. These data were used to design a molecular assay targeting markers that are shared among serotypes noted for being invasive and/or causing the most human illnesses (i.e. Highly Pathogenic *Salmonella* or HPS) but are notably absent among serotypes with a lower frequency of association with human illness (Table 1).

Multiplex PCR Assay to identify Highly Pathogenic Salmonella (HPS)

| | Serotype | n | HPS-6 | HPS-1 | HPS-3 | HPS-5 | HPS-4 | HPS-2 | invA | number of |
|---------|-------------------------------|------|-------|-------|-------|-------|-------|-------|-------|------------------|
| | size (bp) | | | | | | | | | targets detected |
| DENT | Typhimurium | 171 | 99.4 | 28.1 | 100.0 | 100.0 | 69.6 | 100.0 | 100.0 | 5-7 |
| | Dublin | 44 | 4.5 | 100.0 | 100.0 | 95.5 | 88.6 | 100.0 | 100.0 | 5-6 |
| <u></u> | Enteritidis (80%) | 24 | 0.0 | 8.3 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 5-6 |
| \Box | Newport (93%) | 172 | 100.0 | 2.3 | 100.0 | 100.0 | 0.0 | 99.4 | 100.0 | 5-6 |
| L | 1,4,[5],12:i:- | 14 | 100.0 | 0.0 | 100.0 | 100.0 | 0.0 | 100.0 | 100.0 | 5-6 |
| | Heidleberg | 22 | 100.0 | 4.5 | 100.0 | 100.0 | 0.0 | 0.0 | 100.0 | 4 |
| | Newport* (7%) | 12 | 100.0 | 0.0 | 83.3 | 100.0 | 0.0 | 16.7 | 100.0 | 3-4 |
| | Lubbock | 65 | 100.0 | 0.0 | 98.5 | 100.0 | 0.0 | 0.0 | 100.0 | 3-4 |
| | Mbandaka | 39 | 97.4 | 0.0 | 100.0 | 100.0 | 0.0 | 0.0 | 100.0 | 3-4 |
| | Infantis | 19 | 78.9 | 0.0 | 94.7 | 94.7 | 0.0 | 15.8 | 100.0 | 3-4 |
| | Muenchen | 12 | 91.7 | 0.0 | 91.7 | 91.7 | 0.0 | 0.0 | 100.0 | 3-4 |
| | Thompson | 11 | 9.1 | 9.1 | 90.9 | 90.9 | 0.0 | 54.5 | 100.0 | 3-4 |
| | Kentucky | 56 | 60.7 | 0.0 | 96.4 | 94.6 | 0.0 | 0.0 | 100.0 | 3-4 |
| | Enteritidis* (20%) | 6 | 0.0 | 0.0 | 66.7 | 83.3 | 0.0 | 83.3 | 100.0 | 3-4 |
| | Meleagridis | 32 | 0.0 | 0.0 | 100.0 | 100.0 | 0.0 | 0.0 | 100.0 | 3 |
| | Agona | 28 | 0.0 | 0.0 | 100.0 | 100.0 | 0.0 | 0.0 | 100.0 | 3 |
| | Anatum | 288 | 100.0 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 100.0 | 3 |
| | Lille | 46 | 100.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0 | 100.0 | 3 |
| | Reading | 16 | 87.5 | 0.0 | 12.5 | 75.0 | 0.0 | 12.5 | 100.0 | 3-4 |
| | Montevideo* (4.5%) Clade IV | 7 | 28.6 | 14.3 | 100.0 | 28.6 | 0.0 | 14.3 | 100.0 | 3-4 |
| | Cerro | 205 | 51.7 | 0.0 | 100.0 | 21.0 | 0.0 | 0.0 | 100.0 | 2-3 |
| | Muenster | 59 | 6.8 | 0.0 | 6.8 | 0.0 | 0.0 | 10.2 | 100.0 | 2-3 |
| | Montevideo (95.5%) Clade I | 148 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 1 |
| | EB (39); GB Enrichments (373) | 412 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0 |
| | Total samples tested: | 1908 | | | | | | | | |

Table 1. Salmonella resulting in 5 or more bands are considered HPS. DENT: Dublin, Enteritidis, Newport, Typhimurium. Salmonella with 4 bands are not designated as HPS but have been attributed to outbreaks and can be found on the CDC's list of top 20 Salmonella causing illness in the US. Salmonella with \leq 3 bands are designated as non-HPS and are predicted to be less pathogenic to humans.

To date, the HPS assay has been tested with over 1600 *Salmonella* isolates encompassing 78 serotypes. Preliminary validation testing using *Enterobacteriaceae* of various genera (n=39) has shown no cross reactivity for the assay. The assay was found to have 99% specificity and 96% sensitivity for identifying serotypes Dublin, Enteritidis, Newport and Typhimurium and use of the assay to identify *Salmonella* in > 400 ground beef enrichments showed no cross reactivity.

Salmonellosis results from the interplay of a number of factors including host immune status, infectious dose and *Salmonella* pathogenicity level. As such, mitigation strategies for *Salmonella* contamination in foods should include a quantitative assessment of both contamination level and pathogenicity level (Figure 1). The USDA-ARS is seeking an industry partner to help develop the HPS assay for application in the meat industry, to help identify *Salmonella* pathogenicity level. The ideal CRADA partner would have expertise in developing and marketing a rapid test for detecting pathogens in food and an interest in supporting the project both intellectually and financially.

Step 1. Salmonella contamination? No Step 2. Contamination level? ≤0.1cfu/g Not detected ≥0.1cfu/g ≤1cfu/g ≥1cfu/g **Human Food Safety Risk** Low Step 3. Salmonella Pathogenicity level? **HPS Assay** 1 -3 targets detected - 7 targets detected 4 targets detected Non-HPS Possible HPS **DENT or HPS**

Figure 1. Salmonella risk mitigation strategy.

For more information contact:

Dr. Dayna M. Harhay
US Meat Animal Research Center
402-762-4343
dayna.harhay@usda.gov